

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: December 11, 2006, 20:06:08 ; Search time 174.137 Seconds
(without alignments)
855.952 Million cell updates/sec

Title: US-10-784-721-9
Perfect score: 1731
Sequence: 1 KRCAGNFDSEERSWYNGR.....SCCGXGLEVLFGQPVKXGK 326

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_8.*

- 1: Geneseqp1980a.*
- 2: Geneseqp1990a.*
- 3: Geneseqp2000a.*
- 4: Geneseqp2001a.*
- 5: Geneseqp2002a.*
- 6: Geneseqp2003a.*
- 7: Geneseqp2003ba.*
- 8: Geneseqp2004a.*
- 9: Geneseqp2005a.*
- 10: Geneseqp2006a.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1729	99.9	326	10 AEF92390	Aef92390 Biotinyia
2	1691	97.7	318	10 AEF92389	Aef92389 Fluoresce
3	1612	93.1	304	10 AEF10978	Aef10978 Mouse c-C
4	1605	92.7	304	2 AAW05409	Aaw05409 Mouse Crk
5	1605	92.7	304	7 ADE56188	Ade56188 Rat Prote
6	1588	91.7	304	7 ADE56190	Ade56190 Human Pro
7	1588	91.7	304	8 ADJ66607	Adj66607 CRK prote

8	1588	91.7	104	8 ADR99143	Adr99143 v-crck aar
9	1129	65.2	256	2 AAR85919	Aar85919 Human GRB
10	1058	61.1	204	9 ADY68650	Ady68650 Human v-C
11	917.5	53.0	303	2 AAW42071	Aaw42071 Human Crk
12	917.5	53.0	303	9 ADM08737	Adm08737 Human pro
13	917.5	53.0	389	8 ADP48927	Adp48927 Human-her
14	917.5	53.0	443	8 ADP48921	Adp48921 Human-yea
15	917.5	53.0	444	8 ADP48949	Adp48949 Human-yea
16	917.5	53.0	455	8 ADP48947	Adp48947 Human-yea
17	913.5	52.8	303	2 AAR77439	Aar77439 Mouse CRK
18	905.5	52.3	447	8 ADP48913	Adp48913 Human-yea
19	642.5	37.1	271	4 ABB58271	Abb58271 Drosophill
20	387.5	22.4	107	7 ADN11818	Adn11818 v-Crk SH2
21	321	18.5	79	2 AAW54313	Aaw54313 NH2-termi
22	257	14.8	50	3 AAB12071	Aab12071 SH3 domai
23	257	14.8	217	2 AAW18063	Aaw18063 Growth fa
24	257	14.8	217	7 ADG14308	Adg14308 Human Grb
25	257	14.8	217	7 ADN95325	Adn95325 Human BEC
26	251	14.5	50	7 ADE84644	Ade84644 v-crck SH3
27	236	13.6	211	4 ABB62014	Abb62014 Drosophill
28	234.5	13.5	234	8 ADP48915	Adp48915 Human-yea
29	231.5	13.4	211	8 ADP48923	Adp48923 Human-yea
30	231.5	13.4	212	8 ADP48950	Adp48950 Human-yea
31	230	13.3	211	8 ADP48917	Adp48917 Human-yea
32	228	13.2	158	8 ADP48929	Adp48929 Human-her
33	224	12.9	217	2 AAR85918	Aar85918 Human GRB
34	224	12.9	217	2 AAW14004	Aaw14004 Human GRB
35	224	12.9	217	2 AAW42070	Aaw42070 Growth fa
36	224	12.9	217	5 ABB57107	Abb57107 Mouse isc
37	224	12.9	217	7 ADD18644	Add18644 Human dis
38	224	12.9	217	7 ADE56262	Ade56262 Human pro
39	224	12.9	217	7 ADD45298	Add45298 Human pro
40	224	12.9	217	7 ADD45296	Add45296 Rat Prote
41	224	12.9	217	7 ADE58870	Ade58870 Rat Prote
42	224	12.9	217	7 ADE58872	Ade58872 Human pro
43	224	12.9	217	7 ADE56260	Ade56260 Rat Prote
44	224	12.9	217	8 ADJ66547	Adj66547 Grb2 prot
45	224	12.9	217	8 ABBM81927	Abm81927 Tumour-ag

ALIGNMENTS

RESULT 1
AEF92390
ID AEF92390 standard; protein; 326 AA.
XX
AC AEF92390;
XX

DT 20-APR-2006 (first entry)

XX Biotinylated fluorescein-labeled mouse ABL tyrosine kinase.
DE
XX
XX
KW enzyme; protein engineering; protein kinetics; protein interaction;
KW phosphorylation; dephosphorylation; fluorescence; fusion protein; sensor;
KW Abelson murine leukemia viral oncogene homolog tyrosine kinase;
KW ABL tyrosine kinase; cell signaling.

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OM protein - protein search, using sw model

Run on: December 11, 2006, 20:06:57 ; Search time 196.916 Seconds
(without alignments)
1531.388 Million cell updates/sec

Title: US-10-784-721-9

Perfect score: 1731

Sequence: 1 KRCCAGNFDSEERSWYGR.....SCGXGLVLFQGPVRKXG 326

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Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_7.2.*

1: uniprot_sprot.*

2: uniprot_trembl.*

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1612	93.1	304	1 CRK_MOUSE	Q64010 mus musculus
2	1612	93.1	304	2 Q5ND51_MOUSE	Q5nd51 m v-crck sar
3	1609	93.0	304	2 Q96HJ0_HUMAN	Q96hj0 homo sapien
4	1605	92.7	304	1 CRK_RAT	Q63768 rattus norv
5	1594	92.1	304	2 Q91VM1_MOUSE	Q91vm1 mus musculus
6	1588	91.7	304	1 CRK_HUMAN	P46108 homo sapien
7	1379.5	79.7	305	1 CRK_CHICK	Q04929 gallus gall
8	1361	78.6	257	2 Q8BPE7_MOUSE	Q8bpe7 mus musculus
9	1357	78.4	296	2 Q6GLF5_XENTR	Q6glf5 xenopus tro
10	1353	78.2	283	2 Q920I1_MOUSE	Q920i1 mus musculus
11	1315	76.0	296	1 CRK_XENLA	P87378 xenopus lae
12	1159	67.0	223	2 Q5ND50_MOUSE	Q5nd50 mus musculus
13	1140.5	65.9	311	2 Q6DEM2_BRARE	Q6dem2 brachydanio
14	1078	62.3	239	2 Q9QW60_9MURI	Q9qw60 mus sp. grb
15	1063.5	61.4	333	2 Q4TDQ2_TETNG	Q4tdq2 tetraodon n

16	1061	61.3	204	2	Q8JZR2_MOUSE	Q8jar2 m crk prote
17	1058	61.1	204	2	Q96GA9_HUMAN	Q96ga9 homo sapien
18	1055	60.9	261	2	Q3TTI0_MOUSE	Q3tti0 mus musculus
19	1007	58.2	254	2	Q6PAB9_XENLA	Q6pab9 xenopus lae
20	938	54.2	302	2	Q66KG8_XENLA	Q66kg8 xenopus lae
21	938	54.2	302	2	Q6NTZ1_XENLA	Q6ntz1 xenopus lae
22	925.5	53.5	305	2	Q6PH06_BRARE	Q6ph06 brachydanio
23	917.5	53.0	303	1	CRKL_HUMAN	P46109 homo sapien
24	917.5	53.0	303	2	Q5UZU2_RAT	Q5uzu2 rattus norv
25	913.5	52.8	303	1	CRKL_MOUSE	P47941 mus musculus
26	913.5	52.8	303	2	Q3TQ18_MOUSE	Q3tq18 mus musculus
27	865.5	50.0	295	2	Q48213_TETNG	Q48213 tetraodon n
28	849	49.0	338	2	Q4SW52_TETNG	Q4sw52 tetraodon n
29	836.5	48.3	249	2	Q4TEX3_TETNG	Q4tex3 tetraodon n
30	834.5	48.2	255	2	Q99059_9RETR	Q99059 avian sarco
31	818.5	47.3	440	1	GAGC_AVISC	P05433 avian sarco
32	659.5	38.1	289	2	Q6P8B4_XENTR	Q6p8b4 xenopus tro
33	652.5	37.7	256	2	Q7QG48_ANOGA	Q7qg48 anopheles g
34	642.5	37.1	271	1	CRK_DROME	Q9XYM0 drosophila
35	642.5	37.1	271	2	Q53XD2_DROME	Q53xd2 drosophila
36	591.5	34.2	253	2	Q9SRW2_DROME	Q9srw2 drosophila
37	427	24.7	82	2	Q3TOV3_MOUSE	Q3tov3 mus musculus
38	367.5	21.2	98	2	Q8RSB8_MOUSE	Q8rsb8 mus musculus
39	343	19.8	279	2	Q9NHC3_CABEL	Q9nhc3 caenorhabdi
40	333	19.2	277	2	Q61AY7_CABER	Q61ay7 caenorhabdi
41	257	14.8	217	1	GRAP_HUMAN	Q13588 homo sapien
42	236	13.6	211	1	DRK_DROME	Q08012 drosophila
43	236	13.6	211	1	DRK_DROSI	Q6YK48 drosophila
44	233	13.5	211	2	Q7PV64_ANOGA	Q7pv64 anopheles g
45	229	13.2	217	1	GRAP_MOUSE	Q9CX99 mus musculus

ALIGNMENTS

RESULT 1

CRK_MOUSE
ID CRK_MOUSE STANDARD; PRT; 304 AA.
AC Q64010;
DT 01-NOV-1997, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1996, sequence version 1.
DT 07-MAR-2006, entry version 51.
DE Proto-oncogene C-crck (P38) (Adapter molecule crk).
GN Names=Crk; Synonyms=Crko;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS CRK-I AND CRK-II).
RC TISSUE=Liver;
RX MEDLINE=94239744; PubMed=8183562;
RA Ogawa S., Toyoshima H., Kozutsumi H., Hagiwara K., Sakai R.,
RA Tanaka T., Hirano N., Mano H., Yazaki Y., Hirai H.;
RT "The C-terminal SH3 domain of the mouse c-Crk protein negatively
regulates tyrosine-phosphorylation of Crk associated p130 in rat 3Y1

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OM protein - protein search, using sw model

Run on: December 11, 2006, 20:12:59 ; Search time 26.8292 Seconds
(without alignments)
1169.124 Million cell-updates/sec

Title: US-10-784-721-9

Perfect score: 1731

Sequence: 1 KRGCAGNFDSEERSMYWGR.....SOGXGGLVLPQGVKXG 326

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_80.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1612	93.1	304	2 158394	C-Crk - mouse
2	1588	91.7	304	2 A45022	CRK-II - human
3	1379.5	79.7	305	1 A49011	C-Crk - chicken
4	1078	62.3	239	2 A46243	epidermal growth f
5	1052	60.8	204	2 B45022	CRK-I - human
6	917.5	53.0	303	2 S41754	CRKL protein - hum
7	911.5	52.7	303	2 S58352	SH2/SH3 adaptor pr
8	834.5	48.2	259	2 A44988	transforming prote
9	818.5	47.3	232	1 TVFV10	transforming prote
10	216	13.6	211	2 A46444	SH2-SH3 adaptor pr
11	224	12.9	217	2 A43221	growth factor rece
12	224	12.9	217	2 A54688	modular adaptor Gr
13	224	12.9	217	2 S26050	growth factor rece

14	218	12.6	217	2 JT0664	growth factor rece
15	202	11.7	228	2 S25730	SH2-SH3 protein se
16	184	10.6	1291	2 S00666	1-phosphatidylinos
17	182	10.5	1097	2 T31504	hypothetical prote
18	178	10.3	1290	2 A36466	1-phosphatidylinos
19	177	10.2	1290	2 A31317	1-phosphatidylinos
20	172.5	10.0	839	1 TVH0V	transforming prote
21	170	9.8	816	2 T17257	hypothetical prote
22	167	9.6	844	1 TVMSV	transforming prote
23	165	9.5	1270	2 T09194	adaptor protein in
24	164	9.5	1196	2 T14108	SH3-containing pro
25	161	9.3	1094	2 T13053	dynamn associated
26	158.5	9.2	330	2 JE0376	Grb-2 related adap
27	154.5	8.9	878	2 T51940	gene VAV2 protein
28	152.5	8.8	1011	2 T13055	dynamn associated
29	151.5	8.8	334	2 T33836	hypothetical prote
30	151	8.7	1168	1 MWXIC	myosin heavy chain
31	150	8.7	443	2 T27877	hypothetical prote
32	150	8.7	960	1 A39651	discs-large tumor
33	149.5	8.6	639	2 T13151	adaptor protein CM
34	148.5	8.6	1113	1 A47106	myosin heavy chain
35	148	8.5	290	2 T42526	hypothetical prote
36	147	8.5	1044	2 S01966	GTPase-activating
37	146.5	8.5	1038	2 JT0663	ras GTPase-activat
38	146	8.4	946	2 T38100	rho-GTPase-activat
39	144.5	8.3	1047	2 A40121	GTPase-activating
40	143.5	8.3	870	2 B40121	GTPase-activating
41	142	8.2	450	2 A41973	protein-tyrosine k
42	141	8.1	665	2 JC7191	85K c-Cbl-interact
43	139.5	8.1	1236	1 A53970	1-phosphatidylinos
44	139	8.0	359	2 S27788	neutrophil oxidase
45	139	8.0	1196	2 T23832	protein-tyrosine k

ALIGNMENTS

RESULT 1

I58394
C-Crk - mouse
C:Species: Mus sp. (mouse)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999
C:Accession: I58394
R:Ogawa, S.; Toyoshima, H.; Kozutsumi, H.; Hagiwara, K.; Sakai, R.; Tanaka, T.; Hirano, N.; Mano, H.; Yazaki, Y.; Hirai, H.
Oncogene 9, 1669-1678, 1994
A:Title: The C-terminal SH3 domain of the mouse c-Crk protein negatively regulates tyrosine-phosphorylation of Crk associated p130 in rat 3Y1 cells.
A:Reference number: I58394; MUID:94239744; PMID:8183562
A:Accession: I58394
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-304 <RES>
A:Cross-references: UNIPARC:UPI00000003F6F; GB:S72408; NID:G632866; PIDN:AB30755.1; PID:G632867
C:Genetics:
C:Gene: c-crk

OM protein - protein search, using sw model

Run on: December 11, 2006, 20:06:08 ; Search time 169.863 Seconds
(without alignments)
855.952 Million cell updates/sec

Title: US-10-784-721-8

Perfect score: 1692

Sequence: 1 KRGCAGNFDSERSWTWGR.....QQNPDEDFSGCGKLEVLFP 318

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq.8.*
1: geneseqp1980s.*
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3: geneseqp2000s.*
4: geneseqp2001s.*
5: geneseqp2002s.*
6: geneseqp2003as.*
7: geneseqp2003bs.*
8: geneseqp2004s.*
9: geneseqp2005s.*
10: geneseqp2006s.*

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5	1605	94.9	304	7 ADE56188	Ade56188 Rat Prote
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12	917.5	54.2	303	9	ADM08737	Adm08737 Human Pro
13	917.5	54.2	389	8	ADP48927	Adp48927 Human-her
14	917.5	54.2	443	8	ADP48921	Adp48921 Human-yea
15	917.5	54.2	444	8	ADP48949	Adp48949 Human-yea
16	917.5	54.2	455	8	ADP48947	Adp48947 Human-yea
17	913.5	54.0	303	2	AAR77439	Aar77439 Mouse CRK
18	905.5	53.5	447	8	ADP48913	Adp48913 Human-yea
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28	234.5	13.9	234	8	ADP48915	Adp48915 Human-yea
29	231.5	13.7	211	8	ADP48923	Adp48923 Human-yea
30	231.5	13.7	212	8	ADP48950	Adp48950 Human-yea
31	230	13.6	211	8	ADP48917	Adp48917 Human-yea
32	228	13.5	158	8	ADP48929	Adp48929 Human-her
33	224	13.2	217	2	AAR85918	Aar85918 Human GRB
34	224	13.2	217	2	AAW14004	Aaw14004 Human GRB
35	224	13.2	217	2	AAW42070	Aaw42070 Growth fa
36	224	13.2	217	5	AB57107	Ab57107 Mouse isc
37	224	13.2	217	7	ADD18644	Add18644 Human dis
38	224	13.2	217	7	ADE56262	Ade56262 Human Pro
39	224	13.2	217	7	ADD45298	Add45298 Human Pro
40	224	13.2	217	7	ADD45296	Add45296 Rat Prote
41	224	13.2	217	7	ADE58870	Ade58870 Rat Prote
42	224	13.2	217	7	ADE58872	Ade58872 Human Pro
43	224	13.2	217	7	ADE56260	Ade56260 Rat Prote
44	224	13.2	217	8	ADJ66547	Adj66547 Grb2 prot
45	224	13.2	217	8	ABM81927	Abm81927 Tumout-ag

ALIGNMENTS

RESULT 1

AEF92389
ID AEF92389 standard; protein; 318 AA.

XX

XX AEF92389;

AC

XX AEF92389;

DT 20-APR-2006 (first entry)

XX Fluorescein-labeled mouse Abl tyrosine kinase.

DE enzyme; protein engineering; protein kinetics; protein interaction;

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Run on: December 11, 2006, 20:06:57 ; Search time 192.084 Seconds
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4	1605	94.9	304	1 CRK_RAT	Q63768 rattus norv
5	1594	94.2	304	2 Q91VM1_MOUSE	Q91vm1 mus musculus
6	1588	93.9	304	1 CRK_HUMAN	P46108 homo sapien
7	1379.5	81.5	305	1 CRK_CHICK	Q04929 gallus gall
8	1361	80.4	257	2 Q8BEF7_MOUSE	Q8bpe7 mus musculus
9	1357	80.2	296	2 Q6GLF5_XENTR	Q6glf5 xenopus tro
10	1353	80.0	283	2 Q920I1_MOUSE	Q920i1 mus musculus
11	1315	77.7	296	1 CRK_XENLA	P87378 xenopus lae
12	1159	68.5	223	2 Q5ND50_MOUSE	Q5nd50 mus musculus
13	1140.5	67.4	311	2 Q6DEM2_BRARE	Q6dem2 brachydanio
14	1078	63.7	239	2 Q9QW60_9MURI	Q9qw60 mus sp. grb
15	1063.5	62.9	333	2 Q4TDQ2_TETNG	Q4tdq2 tetraodon n

16	1061	62.7	204	2 Q8JZR2_MOUSE	Q8jzr2 m crk prote
17	1058	62.5	204	2 Q96GA9_HUMAN	Q96ga9 homo sapien
18	1055	62.4	261	2 Q3T710_MOUSE	Q3tt10 mus musculu
19	1007	59.5	254	2 Q6PAB9_XENLA	Q6pab9 xenopus lae
20	938	55.4	302	2 Q66KG8_XENLA	Q66kg8 xenopus lae
21	938	55.4	302	2 Q6NTZ1_XENLA	Q6ntz1 xenopus lae
22	925.5	54.7	305	2 Q6PH06_BRARE	Q6ph06 brachydanio
23	917.5	54.2	303	1 CRKL_HUMAN	P46109 homo sapien
24	917.5	54.2	303	2 Q5U7U2_RAT	Q5u7u2 rattus norv
25	913.5	54.0	303	1 CRKL_MOUSE	P47941 mus musculu
26	913.5	54.0	303	2 Q3TQ18_MOUSE	Q3tq18 mus musculu
27	865.5	51.2	295	2 Q4RZ13_TETNG	Q4rz13 tetraodon n
28	849	50.2	338	2 Q4SW52_TETNG	Q4sw52 tetraodon n
29	836.5	49.4	249	2 Q4TEX3_TETNG	Q4tex3 tetraodon n
30	834.5	49.3	255	2 Q99059_9RETR	Q99059 avian sarco
31	818.5	48.4	440	1 GAGC_AVISC	P05433 avian sarco
32	659.5	39.0	289	2 Q6P8B4_XENTR	Q6p8b4 xenopus tro
33	652.5	38.6	256	2 Q7QG48_ANOGA	Q7qg48 anopheles g
34	642.5	38.0	271	1 CRK_DROME	Q9xymo drosophila
35	642.5	38.0	271	2 Q53XD2_DROME	Q53xd2 drosophila
36	591.5	35.0	253	2 Q95RW2_DROME	Q95rw2 drosophila
37	427	25.2	82	2 Q3TOV3_MOUSE	Q3tov3 mus musculu
38	367.5	21.7	98	2 Q8RSB8_MOUSE	Q8rsb8 mus musculu
39	343	20.3	279	2 Q9NHC3_CABEL	Q9nhc3 caenorhabdi
40	333	19.7	277	2 Q61AY7_CABER	Q61ay7 caenorhabdi
41	257	15.2	217	1 GRAP_HUMAN	Q13588 homo sapien
42	236	13.9	211	1 DRK_DROME	Q08012 drosophila
43	236	13.9	211	1 DRK_DROSI	Q5ykaa drosophila
44	233	13.8	211	2 Q7PV64_ANOGA	Q7pv64 anopheles g
45	229	13.5	217	1 GRAP_MOUSE	Q9cpx9 mus musculu

ALIGNMENTS

RESULT 1

CRK_MOUSE
ID CRK_MOUSE STANDARD; PRT; 304 AA.
AC Q64010;
DT 01-NOV-1997, integrated into UniProtKB/Swiss-Prot.
DT 07-MAR-2006, entry version 51.
DE Proto-oncogene C-crck (P38) (adapter molecule crk).
GN Name=Crk; Synonyms=Crko;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS CRK-I AND CRK-II).
RC TISSUE=Liver;
RA Ogawa S., Toyoshima H., Kozutsumi H., Hagiwara K., Sakai R.,
RA Tanaka T., Hirano N., Mano H., Yazaki Y., Hirai H.,
RT "The C-terminal SH3 domain of the mouse c-Crk protein negatively
regulates tyrosine-phosphorylation of Crk associated p130 in rat 3Y1

OM protein - protein search, using sw model

Run on: December 11, 2006, 20:12:59 ; Search time 26.1708 Seconds
(without alignments)
1169.124 Million cell updates/sec

Title: US-10-784-721-8

Perfect score: 1692

Sequence: 1 KRGCAGNFDSEERSWYGR.....QQNPDEDFSGCGXGLEVLQ 318

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1612	95.3	304	2 158394	C-Crk - mouse
2	1588	93.9	304	2 A45022	CRK-II - human
3	1379.5	81.5	305	1 A49011	C-Crk - chicken
4	1078	63.7	239	2 A46243	epidermal growth f
5	1052	62.2	204	2 B45022	CRK-I - human
6	917.5	54.2	303	2 S41754	CRKL protein - hum
7	911.5	53.9	303	2 S58352	SH2/SH3 adaptor pr
8	834.5	49.3	259	2 A44988	transforming prote
9	818.5	48.4	232	1 TVFV10	transforming prote
10	236	13.9	211	2 A46444	SH2-SH3 adaptor pr
11	224	13.2	217	2 A43321	growth factor rece
12	224	13.2	217	2 A54688	modular adaptor Gr
13	224	13.2	217	2 S26050	growth factor rece

ALIGNMENTS

RESULT 1

158394

C-Crk - mouse

C.Species: Mus sp. (mouse)

C.Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999

C.Accession: 158394

R.Ogawa, S.; Toyoshima, H.; Kozutsumi, H.; Hagiwara, K.; Sakai, R.; Tanaka, T.;

Hirano, N.; Mano, H.; Yazaki, Y.; Hirai, H.

Oncogene 9, 1669-1678, 1994

A>Title: The C-terminal SH3 domain of the mouse c-Crk protein negatively
regulates tyrosine-phosphorylation of Crk associated p130 in rat 3Y1 cells.

A.Reference number: 158394; MUID:94239744; PMID:8183562

A.Accession: 158394

A.Status: preliminary; translated from GB/EMBL/DDBJ

A.Molecule type: mRNA

A.Residues: 1-304 <RES>

A.Cross-references: UNIPARC:UPI0000003f6f; GB:S72408; NID:g632866;

PIDN:AB30755.1; PID:g632867

C.Genetics:

A.Gene: C-crk

14	218	12.9	217	2	JT0664	growth factor rece
15	202	11.9	228	2	S25730	SH2-SH3 protein se
16	184	10.9	1291	2	S00666	1-phosphatidylinos
17	182	10.8	1097	2	T31504	hypothetical prote
18	178	10.5	1290	2	A36466	1-phosphatidylinos
19	177	10.5	1290	2	A31317	1-phosphatidylinos
20	172.5	10.2	839	1	TVROVV	transforming prote
21	170	10.0	816	2	T17257	hypothetical prote
22	167	9.9	844	1	TVMSVV	transforming prote
23	165	9.8	1270	2	T09194	adaptor protein in
24	164	9.7	1196	2	T14108	SH3-containing pro
25	161	9.5	1094	2	T13053	dynamain associated
26	158.5	9.4	330	2	JE0376	Grb-2 related adap
27	154.5	9.1	878	2	I51940	gene VAV2 protein
28	152.5	9.0	1011	2	T13055	dynamain associated
29	151.5	9.0	334	2	T33836	hypothetical prote
30	151	8.9	1168	1	MWAXIC	myosin heavy chain
31	150	8.9	960	1	A39651	discs-large tumor
32	149	8.8	639	2	T13151	adaptor protein CM
33	148.5	8.8	1113	1	A47106	myosin heavy chain
34	148	8.7	290	2	T42526	hypothetical prote
35	148	8.7	443	2	T27877	hypothetical prote
36	147	8.7	1044	2	S01966	GTPase-activating
37	146.5	8.7	1038	2	JT0663	ras GTPase-activat
38	146	8.6	946	2	I38100	rho-GTPase-activat
39	144.5	8.5	1047	2	A40121	GTPase-activating
40	143.5	8.5	870	2	B40121	GTPase-activating
41	142	8.4	450	2	A41973	protein-tyrosine k
42	141	8.3	665	2	JC7191	85K c-Cbl-interact
43	139.5	8.2	1236	1	A53970	1-phosphatidylinos
44	139	8.2	359	2	S27788	neutrophil oxidase
45	139	8.2	1196	2	T23832	protein-tyrosine k